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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=1; day=14; hr=11; min=45; sec=0; ms=652;]

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Application No: 10500240 Version No: 4.0

Input Set:**Output Set:**

Started: 2008-12-31 11:18:48.658
Finished: 2008-12-31 11:18:55.043
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 385 ms
Total Warnings: 23
Total Errors: 30
No. of SeqIDs Defined: 106
Actual SeqID Count: 106

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

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Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (24)
E 257	Invalid sequence data feature in <221> in SEQ ID (24)
E 257	Invalid sequence data feature in <221> in SEQ ID (26)
E 257	Invalid sequence data feature in <221> in SEQ ID (36)
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E 257	Invalid sequence data feature in <221> in SEQ ID (42)
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E 257	Invalid sequence data feature in <221> in SEQ ID (56)
E 257	Invalid sequence data feature in <221> in SEQ ID (58)
E 257	Invalid sequence data feature in <221> in SEQ ID (60)
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E 257	Invalid sequence data feature in <221> in SEQ ID (78)
	This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> WILDT, Stefan
MIELE, Robert G.
NETT, Juergen H.
DAVIDSON, Robert C.

<120> METHODS TO ENGINEER MAMMALIAN-TYPE
CARBOHYDRATE STRUCTURES

<130> GF0022P

<140> 10500240
<141> 2005-03-23

<150> PCT/US02/41510
<151> 2002-12-24

<150> 60/344,169
<151> 2001-12-27

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 <210> 24
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Leu	Ile	Phe	Trp	Ser	Gly	Met	Pro	Phe	Phe	Val	Gly	Pro	Ile	Trp	Tyr
385					390					395					400
Val	Leu	His	Glu	Trp	Cys	Trp	Asn	Ser	Tyr	Pro	Pro	Asn	Ser	Gln	Xaa
				405					410					415	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			420					425					430		
Xaa	Xaa	Xaa	Xaa	Ser	Gly	Ser	Val	Ala	Leu	Ala	Lys	Ser	His	Leu	Arg
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	450					455									

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<211> 458

<212> PRT

<213> *Saccharomyces cerevisiae*

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Gln	Phe	Val	Arg	Pro	Pro	Leu	Asp	Leu	Trp	Gln	Asp	Leu	Lys	Asp	Gly
		20					25					30			
Val	Arg	Tyr	Val	Ile	Phe	Asp	Cys	Arg	Ala	Asn	Leu	Ile	Val	Met	Pro
	35					40					45				
Leu	Leu	Ile	Leu	Phe	Glu	Ser	Met	Leu	Cys	Lys	Ile	Ile	Ile	Lys	Lys
	50					55				60					
Val	Ala	Tyr	Thr	Glu	Ile	Asp	Tyr	Lys	Ala	Tyr	Met	Glu	Gln	Ile	Glu
65					70				75					80	
Met	Ile	Gln	Leu	Asp	Gly	Met	Leu	Asp	Tyr	Ser	Gln	Val	Ser	Gly	Gly
			85					90				95			
Thr	Gly	Pro	Leu	Val	Tyr	Pro	Ala	Gly	His	Val	Leu	Ile	Tyr	Lys	Met
		100						105				110			
Met	Tyr	Trp	Leu	Thr	Glu	Gly	Met	Asp	His	Val	Glu	Arg	Gly	Gln	Val
	115					120					125				
Phe	Phe	Arg	Tyr	Leu	Tyr	Leu	Leu	Thr	Leu	Ala	Leu	Gln	Met	Ala	Cys
	130					135				140					
Tyr	Tyr	Leu	Leu	His	Leu	Pro	Pro	Trp	Cys	Val	Val	Leu	Ala	Cys	Leu
145				150					155					160	
Ser	Lys	Arg	Leu	His	Ser	Ile	Tyr	Val	Leu	Arg	Leu	Phe	Asn	Asp	Cys
		165						170				175			
Phe	Thr	Thr	Leu	Phe	Met	Val	Val	Thr	Val	Leu	Gly	Ala	Ile	Val	Ala
		180						185				190			
Ser	Arg	Cys	His	Gln	Arg	Pro	Lys	Leu	Lys	Lys	Ser	Leu	Ala	Leu	Val
	195					200					205				
Ile	Ser	Ala	Thr	Tyr	Ser	Met	Ala	Val	Ser	Ile	Lys	Met	Asn	Ala	Leu
	210					215					220				
Leu	Tyr	Phe	Pro	Ala	Met	Met	Ile	Ser	Leu	Phe	Ile	Leu	Asn	Asp	Ala
225				230					235					240	
Asn	Val	Ile	Leu	Thr	Leu	Leu	Asp	Leu	Val	Ala	Met	Ile	Ala	Trp	Gln
			245					250					255		
Val	Ala	Val	Ala	Val	Pro	Phe	Leu	Arg	Ser	Phe	Pro	Gln	Gln	Tyr	Leu
		260						265					270		
His	Cys	Ala	Phe	Asn	Phe	Gly	Arg	Lys	Phe	Met	Tyr	Gln	Trp	Ser	Ile
	275						280					285			
Asn	Trp	Gln	Met	Met	Asp	Glu	Glu	Ala	Phe	Asn	Asp	Lys	Arg	Phe	His

290 295 300
 Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
 305 310 315 320
 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
 325 330 335
 Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
 340 345 350
 Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
 355 360 365
 Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
 370 375 380
 Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
 385 390 395 400
 Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala
 405 410 415
 Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala
 420 425 430
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 435 440 445
 Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
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<212> PRT

<213> *Saccharomyces cerevisiae*

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<222> (333)...(347)

<223> Xaa is a variable amino acid

<400> 26

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 20 25 30
 Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr Thr Glu Ile Asp Tyr Lys
 35 40 45
 Ala Tyr Met Glu Gln Ile Glu Met Ile Gln Leu Asp Gly Met Leu Asp
 50 55 60
 Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Gly
 65 70 75 80
 His Val Leu Ile Tyr Lys Met Met Tyr Trp Leu Thr Glu Gly Met Asp
 85 90 95
 His Val Glu Arg Gly Gln Val Phe Phe Arg Tyr Leu Tyr Leu Leu Thr
 100 105 110
 Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu Leu His Leu Pro Pro Trp
 115 120 125
 Cys Val Val Leu Ala Cys Leu Ser Lys Arg Leu His Ser Ile Tyr Val
 130 135 140
 Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr Leu Phe Met Val Val Thr
 145 150 155 160
 Val Leu Gly Ala Ile Val Ala Ser Arg Cys His Gln Arg Pro Lys Leu
 165 170 175
 Lys Lys His Gln Thr Cys Lys Val Pro Pro Phe Val Phe Phe Phe Met

Cys	Ala	Ser	Tyr	Arg	Val	His	Ser	Ile	Phe	Val	Leu	Arg	Leu	Phe	Asn
130						135					140				
Asp	Pro	Val	Ala	Met	Val	Leu	Leu	Phe	Leu	Ser	Ile	Asn	Leu	Leu	Leu
145					150					155					160
Ala	Gln	Arg	Trp	Gly	Trp	Gly	Cys	Cys	Phe	Phe	Ser	Leu	Ala	Val	Ser
				165					170					175	
Val	Lys	Met	Asn	Val	Leu	Leu	Phe	Ala	Pro	Gly	Leu	Leu	Phe	Leu	Leu
			180					185					190		
Leu	Thr	Gln	Phe	Gly	Phe	Arg	Gly	Ala	Leu	Pro	Lys	Leu	Gly	Ile	Cys
		195					200					205			
Ala	Gly	Leu	Gln	Val	Val	Leu	Gly	Leu	Pro	Phe	Leu	Leu	Glu	Asn	Pro
		210				215				220					
Ser	Gly	Tyr	Leu	Ser	Arg	Ser	Phe	Asp	Leu	Gly	Arg	Gln	Phe	Leu	Phe
225					230					235					